Online-Only Abstracts

Complete genome analyses of G4P[6] rotavirus detected in Argentinean children with diarrhoea provides evidence of interspecies transmission from swine

J. I. Degiuseppe[1], J. C. Beltramino[2], A. Millán[2], J. A. Stupka[1] and and G. I. Parra[3,4]

1) *Instituto Nacional de Enfermedades Infecciosas (ANLIS 'Dr Carlos G. Malbrán'), Buenos Aires, Argentina,* 2) *Hospital de Niños 'Dr Orlando Alassia', Santa Fe, Argentina,* 3) *Instituto de Investigaciones en Ciencias de la Salud, Universidad Nacional de Asunción, Asunción, Paraguay and* 4) *Laboratory of Infectious Diseases, NIH, NIAID, Bethesda, MD, USA*

Original Submission: 13 February 2013; **Accepted:** 6 March 2013
Editor: L. Kaiser
Article published online: 13 March 2013
Clin Microbiol Infect 2013; **19:** E367–E371
10.1111/1469-0691.12216

Abstract

Rotaviruses are dynamic pathogens that have been shown to infect multiple species. In 2006, two G4P[6] rotavirus strains with porcine characteristics were detected in Santa Fe, Argentina. To further characterize and determine the origin of these strains, nearly the full length of their genome was sequenced. While most of the genome segments were from porcine origin, the two strains grouped in different phylogenetic clusters in five out of the 11 genes, suggesting two independent interspecies transmission events. This study expands our knowledge of G4 rotavirus and reinforces the use of complete genome analyses as a key tool for diversity and evolution mechanicisms.

Visual detection of human infection with influenza A (H7N9) virus by subtype-specific reverse transcription loop-mediated isothermal amplification with hydroxynaphthol blue dye

K. Nie[1], X. Zhao[2], X. Ding[1,3]*, X. D. Li[2], S. M. Zou[2], J. F. Guo[2], D. Y. Wang[2], R. B. Gao[2], X. Y. Li[2], W. J. Huang[2], Y. L. Shu[2] and X. J. Ma[1]

1) *Key Laboratory for Medical Virology, Ministry of Health, National Institute for Viral Disease Control and Prevention, Chinese Centre for Disease Control and Prevention,* 2) *WHO Collaborating Centre for Reference and Research on Influenza, Chinese National Influenza Centre, National Institute for Viral Disease Control and Prevention, Chinese Centre for Disease Control and Prevention, Beijing and* 3) *College of Light Industry and Food Sciences, South China University of Technology, Guangzhou, Guangdong, China*

Original Submission: 16 April 2013; **Accepted:** 3 May 2013
Editor: D. Raoult
Article published online: 7 May 2013
Clin Microbiol Infect 2013; **19:** E372–E375
10.1111/1469-0691.12263

Abstract

A rapid and sensitive H7 and N9 subtype-specific reverse transcription loop-mediated isothermal amplification assay was developed respectively for visual detection of human-infected influenza A (H7N9) virus. The reaction was performed in one step in a single tube at 63°C for 60 min with the addition of hydroxynaphthol blue dye before amplification. The detection limits of both subtype-specific assays were comparable to those of validated H7 and N9 real-time PCR assays respectively and no cross-detection was observed with influenza A pandemic H1N1, H3N2, H5N1, H9N2 or influenza B virus. The assays were evaluated further with H7N9 virus-infected clinical specimens.